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1600

1646

RAW SEQUENCE LISTING

DATE: 06/21/2002

PATENT APPLICATION: US/09/445,614B

TIME: 14:07:36

Input Set : A:\T1481.txt

Output Set : N:\CRF3\06212002\I445614B.raw

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JUL 08 2002
TECH CENTER 1600/2900

4 <110> APPLICANT: Bonnert, Timothy Peter
6 <120> TITLE OF INVENTION: HUMAN VANILLOID RECEPTOR-LIKE RECEPTOR
9 <130> FILE REFERENCE: T1481
11 <140> CURRENT APPLICATION NUMBER: 09/445,614B
12 <141> CURRENT FILING DATE: 1999-12-08
14 <150> PRIOR APPLICATION NUMBER: 9827016.8
15 <151> PRIOR FILING DATE: 1998-12-08
17 <160> NUMBER OF SEQ ID NOS: 19
19 <170> SOFTWARE: FastSEQ for Windows Version 4.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 2469
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo sapiens
26 <400> SEQUENCE: 1

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28	ggtcctggct	ggaccgagca	gcctcctcct	cctaggatga	cctcaccctc	cagctctcca	120
29	gttttcagg	tggagacatt	agatggaggc	caagaagatg	gctctgaggc	ggacagagga	180
30	aagctggatt	ttgggagcgg	gctgcctccc	atggagtcac	agttccagg	cgaggaccgg	240
31	aaattcgccc	ctcagataag	agtcaacctc	aactaccgaa	agggaaacagg	tgccagtcag	300
32	ccggatccaa	accgatttga	ccgagatcgg	ctcttcaatg	cggtctcccg	gggtgtcccc	360
33	gaggatctgg	ctggacttcc	agagtacctg	agcaagacca	gcaagtacct	caccgactcg	420
34	gaatacacag	agggctccac	aggttaagacg	tgcctgatga	aggctgtgct	gaaccttaag	480
35	gacggagtca	atgcctgcat	tctgccactg	ctgcagatcg	acagggactc	tggcaatcct	540
36	cagcccttgg	taaattgcca	gtgcacagat	gactattacc	gaggccacag	cgctctgcac	600
37	atcgccattg	agaagaggag	tctgcagtgt	gtgaagctcc	tgggtggagaa	tggggccaat	660
38	gtgcatgccc	gggcctgcgg	ccgcttcttc	cagaagggcc	aagggaactg	cttttatttc	720
39	ggtgagctac	ccctctcttt	ggccgcttgc	accaagcagt	gggatgtggt	aagctacctc	780
40	ctggagaacc	cacaccagcc	cgccagcctg	caggccactg	actcccagg	caacacagtc	840
41	ctgcatgccc	tagtgatgat	ctcgacaac	tcagctgaga	acattgcact	ggtgaccagc	900
42	atgtatgatg	ggctcctcca	agctggggcc	cgctcttgcc	ctaccgtgca	gcttgaggac	960
43	atccgcaacc	tgcaggatct	cacgcctctg	aagctggccg	ccaaggagg	caagatcgag	1020
44	attttcaggc	acatcctgca	gcgggagttt	tcaggactga	gccacctttc	ccgaaagtcc	1080
45	accgagtgg	gctatggg	tgccgggtg	tcgctgtatg	acctggcttc	tgtggacagc	1140
46	tgtgaggaga	actcagtgt	ggagatcatt	gcctttcatt	gcaagagccc	gcaccgacac	1200
47	cgaatggtcg	ttttggagcc	cctgaacaaa	ctgctgcagg	cgaaatggga	tctgtctatc	1260
48	cccaagtctt	tcttaaactt	cctgtgtaat	ctgatctaca	tgttcatctt	caccgctggt	1320
49	gcctaccatc	agcctaccct	gaagaagcag	gccgcccctc	acctgaaagc	ggaggttgga	1380
50	aactccatgc	tgtgacggg	ccacatcctt	atcctgctag	gggggatcta	cctcctcggt	1440
51	ggccagctgt	ggtacttctg	gcggcgccac	gtgttcatct	ggatctcggt	catagacagc	1500
52	tactttgaaa	tctcttctct	gttccaggcc	ctgctcacag	tgggtgtcca	ggtgctgtgt	1560
53	ttcctggcca	tcgagtggta	cctgcccctg	cttgtgtctg	cgctgggtgt	gggctggctg	1620
54	aacctgcttt	actatacacg	tggcttccag	cacacaggca	tctacagtgt	catgatccag	1680
55	aagggtcatcc	tgcgggacct	gctgcgcttc	cttctgatct	acttagtctt	ccttttcggc	1740

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56 ttogctgtag ccctggtgag cctgagccag gaggcttggc gccccgaagc tcctacaggc 1800
57 cccaatgcca cagagtcagt gcagcccatg gagggacagg aggacgaggg caacggggcc 1860
58 cagtacaggg gtatcctgga agcctccttg gagctcttca aattcaccat cggcatgggc 1920
59 gagctggcct tccaggagca gctgcacttc cgcggcatgg tgctgctgct gctgctggcc 1980
60 tacgtgctgc tcacctacat cctgctgctc aacatgctca tcgccctcat gagcgagacc 2040
61 gtcaacagtgc tcgccactga cagctggagc atctggaagc tgcagaaagc catctctgtc 2100
62 ctggagatgg agaatggcta ttggtggtgc aggaagaagc agcgggcagg tgtgatgctg 2160
63 accgttggca ctaagccaga tggcagcccg gatgagcgtt ggtgcttcag ggtggaggag 2220
64 gtgaactggg cttcatggga gcagacgctg cctacgctgt gtgaggaccc gtcaggggca 2280
65 ggtgtccctc gaactctcga gaaccctgtc ctggcttccc ctcccaagga ggatgaggat 2340
66 ggtgcctctg aggaaaacta tgtgcccgtc cagctcctcc agtccaactg atggcccaga 2400
67 tgcagcagga ggccagagga cagagcagag gatctttcca accacatctg ctggctctgg 2460
68 ggtccagtc 2469
70 <210> SEQ ID NO: 2
71 <211> LENGTH: 764
72 <212> TYPE: PRT
73 <213> ORGANISM: Homo sapiens
75 <400> SEQUENCE: 2
76 Met Thr Ser Pro Ser Ser Pro Val Phe Arg Leu Glu Thr Leu Asp
77 1 5 10 15
78 Gly Gly Gln Glu Asp Gly Ser Glu Ala Asp Arg Gly Lys Leu Asp Phe
79 20 25 30
80 Gly Ser Gly Leu Pro Pro Met Glu Ser Gln Phe Gln Gly Glu Asp Arg
81 35 40 45
82 Lys Phe Ala Pro Gln Ile Arg Val Asn Leu Asn Tyr Arg Lys Gly Thr
83 50 55 60
84 Gly Ala Ser Gln Pro Asp Pro Asn Arg Phe Asp Arg Asp Arg Leu Phe
85 65 70 75 80
86 Asn Ala Val Ser Arg Gly Val Pro Glu Asp Leu Ala Gly Leu Pro Glu
87 85 90 95
88 Tyr Leu Ser Lys Thr Ser Lys Tyr Leu Thr Asp Ser Glu Tyr Thr Glu
89 100 105 110
90 Gly Ser Thr Gly Lys Thr Cys Leu Met Lys Ala Val Leu Asn Leu Lys
91 115 120 125
92 Asp Gly Val Asn Ala Cys Ile Leu Pro Leu Leu Gln Ile Asp Arg Asp
93 130 135 140
94 Ser Gly Asn Pro Gln Pro Leu Val Asn Ala Gln Cys Thr Asp Asp Tyr
95 145 150 155 160
96 Tyr Arg Gly His Ser Ala Leu His Ile Ala Ile Glu Lys Arg Ser Leu
97 165 170 175
98 Gln Cys Val Lys Leu Leu Val Glu Asn Gly Ala Asn Val His Ala Arg
99 180 185 190
100 Ala Cys Gly Arg Phe Phe Gln Lys Gly Gln Gly Thr Cys Phe Tyr Phe
101 195 200 205
102 Gly Glu Leu Pro Leu Ser Leu Ala Ala Cys Thr Lys Gln Trp Asp Val
103 210 215 220
104 Val Ser Tyr Leu Leu Glu Asn Pro His Gln Pro Ala Ser Leu Gln Ala
105 225 230 235 240
106 Thr Asp Ser Gln Gly Asn Thr Val Leu His Ala Leu Val Met Ile Ser

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107          245          250          255
108 Asp Asn Ser Ala Glu Asn Ile Ala Leu Val Thr Ser Met Tyr Asp Gly
109          260          265          270
110 Leu Leu Gln Ala Gly Ala Arg Leu Cys Pro Thr Val Gln Leu Glu Asp
111          275          280          285
112 Ile Arg Asn Leu Gln Asp Leu Thr Pro Leu Lys Leu Ala Ala Lys Glu
113          290          295          300
114 Gly Lys Ile Glu Ile Phe Arg His Ile Leu Gln Arg Glu Phe Ser Gly
115 305          310          315          320
116 Leu Ser His Leu Ser Arg Lys Phe Thr Glu Trp Cys Tyr Gly Pro Val
117          325          330          335
118 Arg Val Ser Leu Tyr Asp Leu Ala Ser Val Asp Ser Cys Glu Glu Asn
119          340          345          350
120 Ser Val Leu Glu Ile Ile Ala Phe His Cys Lys Ser Pro His Arg His
121          355          360          365
122 Arg Met Val Val Leu Glu Pro Leu Asn Lys Leu Leu Gln Ala Lys Trp
123          370          375          380
124 Asp Leu Leu Ile Pro Lys Phe Phe Leu Asn Phe Leu Cys Asn Leu Ile
125 385          390          395          400
126 Tyr Met Phe Ile Phe Thr Ala Val Ala Tyr His Gln Pro Thr Leu Lys
127          405          410          415
128 Lys Gln Ala Ala Pro His Leu Lys Ala Glu Val Gly Asn Ser Met Leu
129          420          425          430
130 Leu Thr Gly His Ile Leu Ile Leu Leu Gly Gly Ile Tyr Leu Leu Val
131          435          440          445
132 Gly Gln Leu Trp Tyr Phe Trp Arg Arg His Val Phe Ile Trp Ile Ser
133          450          455          460
134 Phe Ile Asp Ser Tyr Phe Glu Ile Leu Phe Leu Phe Gln Ala Leu Leu
135 465          470          475          480
136 Thr Val Val Ser Gln Val Leu Cys Phe Leu Ala Ile Glu Trp Tyr Leu
137          485          490          495
138 Pro Leu Leu Val Ser Ala Leu Val Leu Gly Trp Leu Asn Leu Leu Tyr
139          500          505          510
140 Tyr Thr Arg Gly Phe Gln His Thr Gly Ile Tyr Ser Val Met Ile Gln
141          515          520          525
142 Lys Val Ile Leu Arg Asp Leu Leu Arg Phe Leu Leu Ile Tyr Leu Val
143          530          535          540
144 Phe Leu Phe Gly Phe Ala Val Ala Leu Val Ser Leu Ser Gln Glu Ala
145 545          550          555          560
146 Trp Arg Pro Glu Ala Pro Thr Gly Pro Asn Ala Thr Glu Ser Val Gln
147          565          570          575
148 Pro Met Glu Gly Gln Glu Asp Glu Gly Asn Gly Ala Gln Tyr Arg Gly
149          580          585          590
150 Ile Leu Glu Ala Ser Leu Glu Leu Phe Lys Phe Thr Ile Gly Met Gly
151          595          600          605
152 Glu Leu Ala Phe Gln Glu Gln Leu His Phe Arg Gly Met Val Leu Leu
153          610          615          620
154 Leu Leu Leu Ala Tyr Val Leu Leu Thr Tyr Ile Leu Leu Leu Asn Met
155 625          630          635          640

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156 Leu Ile Ala Leu Met Ser Glu Thr Val Asn Ser Val Ala Thr Asp Ser
 157 645 650 655
 158 Trp Ser Ile Trp Lys Leu Gln Lys Ala Ile Ser Val Leu Glu Met Glu
 159 660 665 670
 160 Asn Gly Tyr Trp Trp Cys Arg Lys Lys Gln Arg Ala Gly Val Met Leu
 161 675 680 685
 162 Thr Val Gly Thr Lys Pro Asp Gly Ser Pro Asp Glu Arg Trp Cys Phe
 163 690 695 700
 164 Arg Val Glu Glu Val Asn Trp Ala Ser Trp Glu Gln Thr Leu Pro Thr
 165 705 710 715 720
 166 Leu Cys Glu Asp Pro Ser Gly Ala Gly Val Pro Arg Thr Leu Glu Asn
 167 725 730 735
 168 Pro Val Leu Ala Ser Pro Pro Lys Glu Asp Glu Asp Gly Ala Ser Glu
 169 740 745 750
 170 Glu Asn Tyr Val Pro Val Gln Leu Leu Gln Ser Asn
 171 755 760

173 <210> SEQ ID NO: 3

174 <211> LENGTH: 51

175 <212> TYPE: DNA

176 <213> ORGANISM: Artificial Sequence

178 <220> FEATURE:

179 <223> OTHER INFORMATION: Primer

181 <400> SEQUENCE: 3

182 tgttaccaat ctgaagtggg agcggcgcgc tcattttttt tttttttttt t

51

184 <210> SEQ ID NO: 4

185 <211> LENGTH: 21

186 <212> TYPE: DNA

187 <213> ORGANISM: Artificial Sequence

189 <220> FEATURE:

190 <223> OTHER INFORMATION: PCR Primer

192 <400> SEQUENCE: 4

193 caggcccggg catgcacatt g

21

195 <210> SEQ ID NO: 5

196 <211> LENGTH: 21

197 <212> TYPE: DNA

198 <213> ORGANISM: Artificial Sequence

200 <220> FEATURE:

201 <223> OTHER INFORMATION: PCR Primer

203 <400> SEQUENCE: 5

204 ccagggcgag gaccggaaat t

21

206 <210> SEQ ID NO: 6

207 <211> LENGTH: 21

208 <212> TYPE: DNA

209 <213> ORGANISM: Artificial Sequence

211 <220> FEATURE:

212 <223> OTHER INFORMATION: PCR Primer

214 <400> SEQUENCE: 6

215 gacagctgga gcatctggaa g

21

217 <210> SEQ ID NO: 7

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218 <211> LENGTH: 21
219 <212> TYPE: DNA
220 <213> ORGANISM: Artificial Sequence
222 <220> FEATURE:
223 <223> OTHER INFORMATION: PCR Primer
225 <400> SEQUENCE: 7
226 gacagctgga gcatctggaa g 21
228 <210> SEQ ID NO: 8
229 <211> LENGTH: 21
230 <212> TYPE: DNA
231 <213> ORGANISM: Artificial Sequence
233 <220> FEATURE:
234 <223> OTHER INFORMATION: PCR Primer
236 <400> SEQUENCE: 8
237 cttccagatg ctccagctgt c 21
239 <210> SEQ ID NO: 9
240 <211> LENGTH: 21
241 <212> TYPE: DNA
242 <213> ORGANISM: Artificial Sequence
244 <220> FEATURE:
245 <223> OTHER INFORMATION: PCR Primer
247 <400> SEQUENCE: 9
248 tttgccacca gaattcactg g 21
250 <210> SEQ ID NO: 10
251 <211> LENGTH: 21
252 <212> TYPE: DNA
253 <213> ORGANISM: Artificial Sequence
255 <220> FEATURE:
256 <223> OTHER INFORMATION: PCR Primer
258 <400> SEQUENCE: 10
259 ctctctttgg ccgcttgac c 21
261 <210> SEQ ID NO: 11
262 <211> LENGTH: 21
263 <212> TYPE: DNA
264 <213> ORGANISM: Artificial Sequence
266 <220> FEATURE:
267 <223> OTHER INFORMATION: PCR Primer
269 <400> SEQUENCE: 11
270 ccagcactga gttctcctca c 21
272 <210> SEQ ID NO: 12
273 <211> LENGTH: 21
274 <212> TYPE: DNA
275 <213> ORGANISM: Artificial Sequence
277 <220> FEATURE:
278 <223> OTHER INFORMATION: PCR Primer
280 <400> SEQUENCE: 12
281 gccctaccgt gcagcttgag g 21
283 <210> SEQ ID NO: 13
284 <211> LENGTH: 21

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VERIFICATION SUMMARY

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